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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/804,625*

DATE: 01/11/2002
TIME: 22:10:28

INPUT SET: S36715.raw

#3

This Raw Listing contains the General Information Section and up to the first 5 pages.

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                        SEQUENCE LISTING

(1)     General Information:

      (i) APPLICANT: Wang, Elizabeth A.
                     Rosen, Vicki A.
                     Wozney, John M

     (ii) TITLE OF INVENTION: Novel BMP Products

    (iii) NUMBER OF SEQUENCES: 6

     (iv) CORRESPONDENCE ADDRESS:
          (A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
          (B) STREET: 87 CAMBRIDGEPARK DRIVE
          (C) CITY: CAMBRIDGE
          (D) STATE: MA
          (E) COUNTRY: USA
          (F) ZIP: 02140

      (v) COMPUTER READABLE FORM:
          (A) MEDIUM TYPE: Floppy disk
          (B) COMPUTER: IBM PC compatible
          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

     (vi) CURRENT APPLICATION DATA:
          (A) APPLICATION NUMBER:   09/804,625
          (B) FILING DATE:
          (C) CLASSIFICATION:

      (vii) PRIOR APPLICATION DATA:
          (A) APPLICATION NUMBER: 08/925,779
          (B) FILING DATE:


   (viii) ATTORNEY/AGENT INFORMATION:
          (A) NAME: Kapinos, Ellen J.
          (B) REGISTRATION NUMBER: 32,245
          (C) REFERENCE/DOCKET NUMBER: 5160C

     (ix) TELECOMMUNICATION INFORMATION:
          (A) TELEPHONE: 617-876-1170
          (B) TELEFAX: 617-876-5851
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(2) INFORMATION FOR SEQ ID NO:1:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 592 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: BOS TAURUS

   (vii) IMMEDIATE SOURCE:
          (A) LIBRARY: BOVINE GENOMIC IN LAMBDA J1
          (B) CLONE: LAMBDA BP-21

  (viii) POSITION IN GENOME:
          (C) UNITS: bp

    (ix) FEATURE:
          (A) NAME/KEY: CDS
          (B) LOCATION: 1..390

    (ix) FEATURE:
          (A) NAME/KEY: mat_peptide
          (B) LOCATION: 46..387


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGC CAC GAT GGG AAA GGA CAC CCT CTC CAC AGA AGA GAA AAG CGG CAA          48
Gly His Asp Gly Lys Gly His Pro Leu His Arg Arg Glu Lys Arg Gln
-15                 -10                  -5                   1

GCA AAA CAC AAA CAG CGG AAA CGC CTC AAG TCC AGC TGT AAG AGA CAC          96
Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His
              5                  10                  15

CCT TTA TAT GTG GAC TTC AGT GAT GTG GGG TGG AAT GAC TGG ATC GTT         144
Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val
         20                  25                  30

GCA CCG CCG GGG TAT CAT GCC TTT TAC TGC CAT GGG GAG TGC CCT TTT         192
Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe
     35                  40                  45

CCC CTG GCC GAT CAC CTT AAC TCC ACG AAT CAT GCC ATT GTC CAA ACT         240
Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr
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 50                 55                  60                  65

CTG GTC AAC TCA GTT AAC TCT AAG ATT CCC AAG GCA TGC TGT GTC CCA       288
Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro
                 70                  75                  80

ACA GAG CTC AGC GCC ATC TCC ATG CTG TAC CTT GAT GAG AAT GAG AAG       336
Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys
             85                  90                  95

GTG GTA TTA AAG AAC TAT CAG GAC ATG GTT GTC GAG GGT TGT GGG TGT       384
Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys
        100                 105                 110

CGT TAGCACAGCA AAATAAAATA TAAATATATA TATATATATA TTAGAAAAAC            437
Arg
    115

AGCAAAAAAA TCAAGTTGAC ACTTTAATAT TTCCCAATGA AGACTTTATT TATGGAATGG     497

AATGGAGAAA AAGAAAAACA CAGCTATTTT GAAAACTATA TTTATATCTA CCGAAAAGAA     557

GTTGGGAAAA CAAATATTTT AATCAGAGAA TTATT                                592


(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 129 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly His Asp Gly Lys Gly His Pro Leu His Arg Arg Glu Lys Arg Gln
-15                 -10                  -5                   1

Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His
              5                  10                  15

Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val
         20                  25                  30

Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe
     35                  40                  45

Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr
 50                 55                  60                  65

Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro
                 70                  75                  80
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Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys
             85                  90                  95

Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys
        100                 105                 110

Arg



(2) INFORMATION FOR SEQ ID NO:3:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1607 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA to mRNA

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (G) CELL TYPE: Osteosarcoma Cell Line
          (H) CELL LINE: U-2OS

   (vii) IMMEDIATE SOURCE:
          (A) LIBRARY: U2OS cDNA in Lambda GT10
          (B) CLONE: Lambda U2OS-39

  (viii) POSITION IN GENOME:
          (C) UNITS: bp

    (ix) FEATURE:
          (A) NAME/KEY: CDS
          (B) LOCATION: 356..1546

    (ix) FEATURE:
          (A) NAME/KEY: mat_peptide
          (B) LOCATION: 1202..1543

    (ix) FEATURE:
          (A) NAME/KEY: mRNA
          (B) LOCATION: 14..1607

    (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 356..424
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    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT       60

AACTTGCGCA CCCCACTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT      120

CCGAGCCCCA CCGCCCCTCC ACTCCTCGGC CTTGCCCGAC ACTGAGACGC TGTTCCCAGC      180

GTGAAAAGAG AGACTGCGCG GCCGGCACCC GGGAGAAGGA GGAGGCAAAG AAAAGGAACG      240

GACATTCGGT CCTTGCGCCA GGTCCTTTGA CCAGAGTTTT TCCATGTGGA CGCTCTTTCA      300

ATGGACGTGT CCCCGCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT CGACC ATG       358
                                                             Met
                                                             -282

GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC CTC        406
Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu
    -280                -275                -270

CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC        454
Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe
-265                -260                -255                -250

GCG GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC        502
Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val
                -245                -240                -235

CTG AGC GAG TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG        550
Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln
            -230                -225                -220

AGA CCC ACC CCC AGC AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC        598
Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp
        -215                -210                -205

CTG TAT CGC AGG CAC TCA GGT CAG CCG GGC TCA CCC GCC CCA GAC CAC        646
Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp His
    -200                -195                -190

CGG TTG GAG AGG GCA GCC AGC CGA GCC AAC ACT GTG CGC AGC TTC CAC        694
Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His
-185                -180                -175                -170

CAT GAA GAA TCT TTG GAA GAA CTA CCA GAA ACG AGT GGG AAA ACA ACC        742
His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr Thr
                -165                -160                -155

CGG AGA TTC TTC TTT AAT TTA AGT TCT ATC CCC ACG GAG GAG TTT ATC        790
Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe Ile
            -150                -145                -140

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